

Reviewer Report

Title: A Single-cell RNA-seq Training and Analysis Suite using the Galaxy Framework

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Reviewer Comments to Author:

1. In the abstract, it would be better if the author could emphasize this Galaxy workflow is only used to 3'-end transcript sequencing. Based on the description of the manuscript, it seems not work on full-transcript sequencing data.
2. In the abstract, 10x Genomics has been mentioned several times, it gives the impression that Galaxy is used to analyze 10x scRNA-seq data. But in the Conclusion of Abstract, the paper mentioned that it works to both 10x and alternative derived datasets. Could you be specific on alternative derived datasets? Does that mean other platform data? The paper addresses the analyses in other platform sequencing.
3. On page 5 of PDF file under 10x Analysis Software category, it describes that 10x Genomics provided software. The software in the paper should be Cell Ranger if I understand it correctly. I could not see Cell Ranger in Galaxy workflow, but found the description in the Methods, which seems STARsolo was used to replace Cell Ranger. I checked on STARsolo paper, which has 95% association with Cell Ranger. A lot of people may prefer to run Cell Ranger for 10x data, it would be great to have Cell Ranger as an option in Galaxy pipeline.
4. On page 9 of PDF file under Pseudotime Techniques, Is PAGA the only technique used in trajectory analysis for Scanpy workflow? There are about 70 methods that can be used to do trajectory analysis, PAGA is not that popular to be selected, is that possible to consider adding other one or two methods to Galaxy?
5. On page 9 of PDF file under Discussion with Cloud-based Analysis. It's a little bit not clear to me. If a user creates Galaxy account, but he/she doesn't have cloud account, is he/she able to run scRNA-seq analysis using Galaxy with cloud computation for free? Galaxy should be a very good user-friendly tool to allow people to use. Due to tremendous number of cells for one study, it may require the large memory and CPU to support the system to run the analysis. If Galaxy is able to solve the computation problem, it would be helpful for the researchers to analyze the data using Galaxy. Please clarify if Galaxy can do the cloud computation, but the academic users also need to pay for the usage or account.
6. The similar question to 5 in Availability of supporting data and materials. UseGalaxy.eu server seems the main server for users to run the analysis, it would be helpful to provide more information, for example, what's the capability for this server in running scRNA-seq data? How many max cells can be run at once in this server?

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